## CLINICAL PROTEOMIC TUMOR ANALYSIS CONSORTIUM

Interrogating Cancer Biology to Address Clinically Relevant Questions



NCI-Clinical Proteomic Tumor Analysis
Consortium: Building A Standardized
Proteogenomic Pipeline for Understanding
Cancer Biology

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National Institutes of Health

## **Clinical Proteomic Tumor Analysis Consortium**

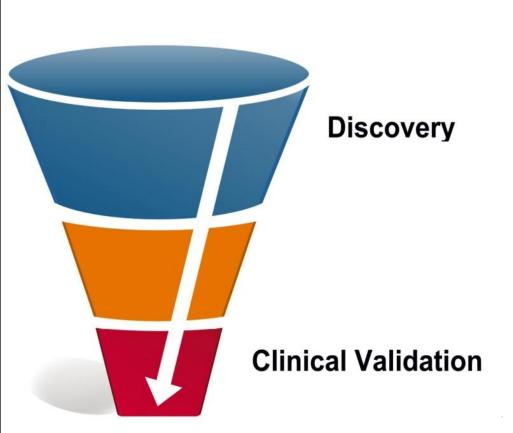


## What is the background?

- Analytical irreproducibility barriers using proteomics (false biomarker claims)
- No FDA-authorized MS-based proteomic assays at the time
- NCI-CPTAC launch in 2006 to address analytical issues
- NCI-TCGA large-scale genomics initiative in 2006 (extensively characterize large number of tumors)

# CPTAC's Multi-stage Standardized Proteomic Pipeline (Building proteomics competency to ensure reproducibility)





### **Round Robin Study Goal:**

Demonstrate MRM assay accuracy and reproducibility across labs to measure proteins in plasma (low ug/ml with CV<22% at LOD)



 Platform Validation (TQMS) using SOPs and common material (research grade), open source software tool Skyline



- Immuno-MRM increases sensitivity by 1000-fold
- Community Adoption

Source: Addona, TA, et. al., Nat Biotechnol. 2009, 27(7):633-641.

# **Analytical Validation Workshop for Regulatory Device Clearance**







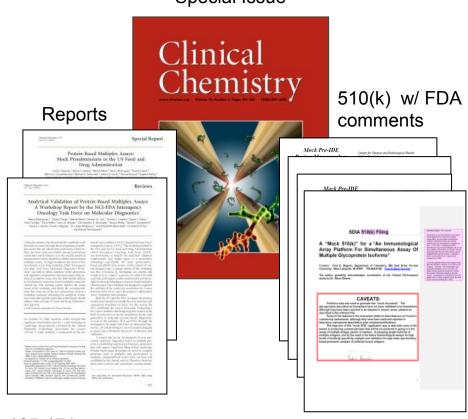
- Workshop (NCI-FDA IOTF MDx subcommittee): analytical validation needs for multiplex proteomic technologies in clinical use
- Outcome: Public mock 510(k)
   pre-market applications
  - multiplex immuno-MRM assay (N. Leigh Anderson)
  - multiplex immunological arraybased assay (Fred Regnier)

#### Sources:

- Regnier, F, et. al. (2010) Clinical Chemistry. 56(2):165-171.
- Rodriguez, H, et. al. (2010) Clinical Chemistry. 56(2):237-243.
- Boja, E, et. al. (2011) Clinical Chemistry. 57(4):1-8.

### Regulatory Science "cliffsnotes"

Special Issue



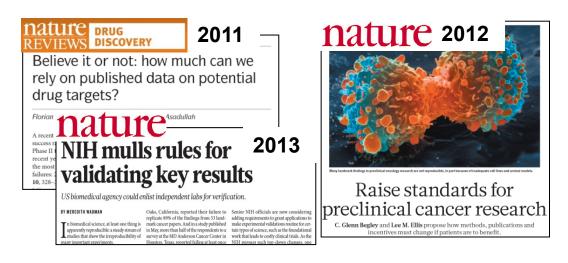
# Fit-for-Purpose Documents (Defining "What Is a Proteomics Targeted Assay")





## What Is an "Assay" (targeted MS)?

- Workshop (2013) establish information authors need to provide to enable reviewers & readers to understand what was done
- Participants: NCI, NHLBI, AACC, FDA, pharma, biotech, CRO, CMS, major journals
- Outcome: fit-for-purpose publication.
  - MCP journal expected to develop recommendations into pub guidelines



Targeted Peptide Measurements in Biology and Medicine:

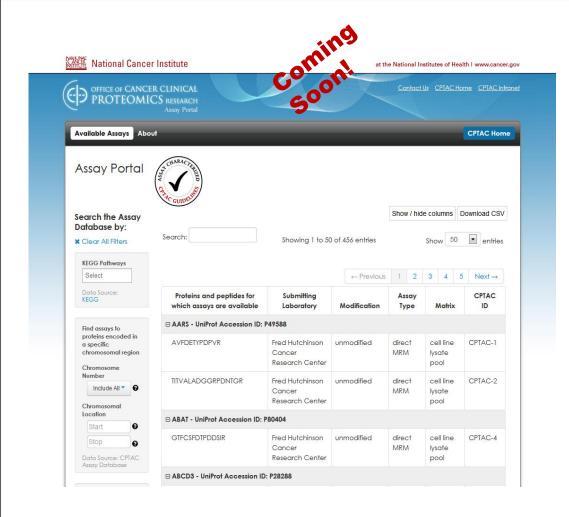
Best Practices for Mass Spectrometry-based Assay Development Using a Fit-for-Purpose Approach

Steven A. Carr<sup>1#</sup>, Susan E. Abbatiello<sup>1</sup>, Bradley L. Ackermann<sup>2</sup>, <sup>3</sup>Christoph Borchers, <sup>4</sup>Bruno Domon, <sup>5</sup>Eric W. Deutsch, <sup>6</sup>Russell P. Grant; <sup>7</sup>Andrew N. Hoofnagle; <sup>8,9</sup>Ruth Hüttenhain; <sup>10</sup>John M. Koomen; <sup>11</sup>Daniel C. Liebler; <sup>12</sup>Tao Liu, <sup>7</sup>Brendan MacLean, <sup>1</sup>DR Mani, <sup>13</sup>Elizabeth Mansfield, <sup>14</sup>Hendrik Neubert, <sup>15</sup>Amanda G. Paulovich, <sup>16</sup>Lukas Reiter, <sup>17</sup>Olga Vitek, <sup>8</sup>Reudi Aebersold, <sup>18</sup>Leigh Anderson, <sup>19</sup>Robert Bethem, <sup>20</sup>Josip Blonder, <sup>20</sup>Emily Boja, <sup>21</sup>Julianne Botelho, <sup>13</sup>Michael Boyne; <sup>9</sup>Ralph A. Bradshaw, <sup>9</sup>Alma L. Burlingame; <sup>22</sup>Daniel Chan; <sup>1</sup>Hasmik Keshishian, <sup>1</sup>Eric Kuhn, <sup>20</sup>Christopher Kinsinger, <sup>20</sup>Jerry Lee, <sup>23</sup>Sang-Won Lee, <sup>5</sup>Robert Moritz, <sup>9</sup>Juan Oses-Prieto, <sup>24</sup>Nader Rifai, <sup>25</sup>James Ritchie, <sup>20</sup>Henry Rodriguez, <sup>26</sup>Pothur R. Srinivas, <sup>27</sup>R. Reid Townsend, <sup>22</sup>Jennifer Van Eyk, <sup>28</sup>Gordon Whiteley, <sup>9</sup>Arun Wiita and <sup>29</sup>Susan Weintraub

Source: Carr, SA, et. al. Targeted Peptide Measurements in Biology and Medicine: Best Practices for Mass Spectrometry-based Assay Development Using a Fit-for-Purpose Approach. (2014) *Mol Cell Proteomics*. 13(3):907-917.

# Alignment of Workshop Guidelines with CPTAC Assay Portal (https://assays.cancer.gov)







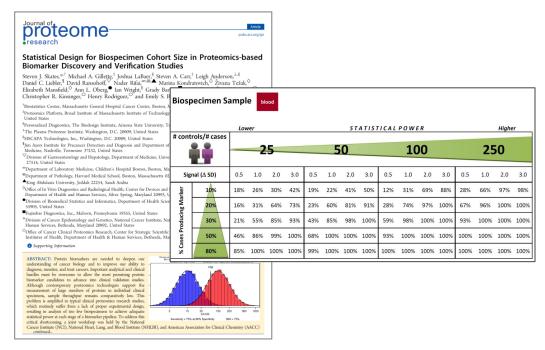
# Experimental and Statistical Study Design Considerations for Discovery and Verification Stages







- Workshop building consensus towards statistically correct biospecimen cohort size when using multiplex proteomic technologies
- Outcome: a peer-reviewed paper (modeling based on CA-125 for cohort size calculation; foundation for tumor analysis)



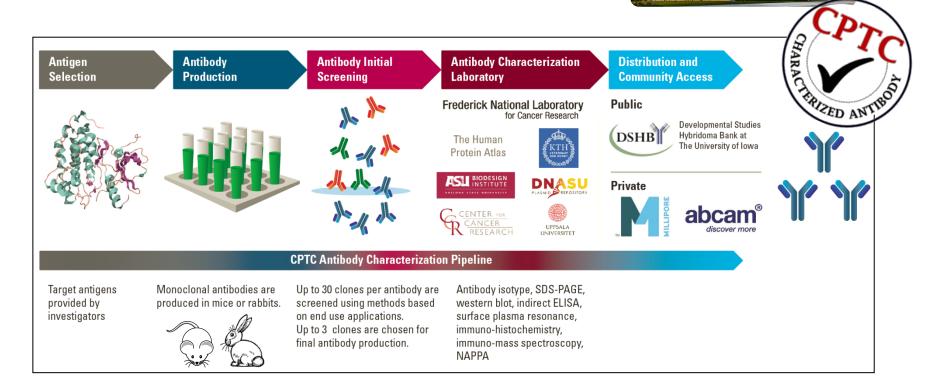
Source: Skates, S, Boja, ES, et. al. Statistical Design for Biospecimen Cohort Size in Proteomics-based Biomarker Discovery and Verification Studies. (2013) *J Proteome Res.* 12(12):5383-5394.

# Community Reagents: Monoclonal Antibodies (Well-characterized / Standardized)



## **Antibody Characterization Program**

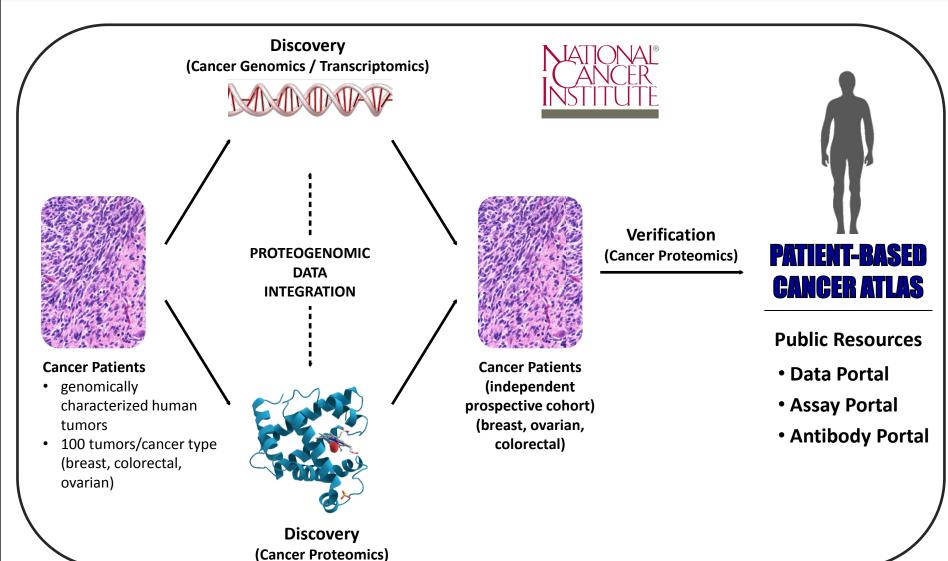
(http://antibodies.cancer.gov)



 Current Inventory: 295 validated monoclonal antibodies (126 full-length protein and peptide antigens)

# Clinical Proteomic Tumor Analysis Consortium: Proteogenomics for Understanding Cancer Biology





## Year 1: Understanding TCGA Pre-analytical Variables



## **Due Diligence Studies**

 Impact of Optimal Cutting Temperature compound on proteomic analysis?



**Outcome** 

Developed OCT removal protocol (no negative impact)

- 2. Accounting for analytical/instrument drift within and among labs?
- Developed CompRef (WHIM breast xenograft) standard allows analytical benchmarking (every 5 TCGA sample runs)

3. Impact of cold ischemia duration on proteome analysis?



Developed consensus tumor collection SOPs for verification set – minimize ischemic effect on proteomic (phospho) analyses

## **Clinical Proteomic Tumor Analysis Consortium**

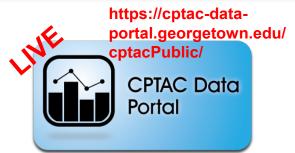


## What has NCI-CPTAC done with FDA/AACC to bridge the gap?

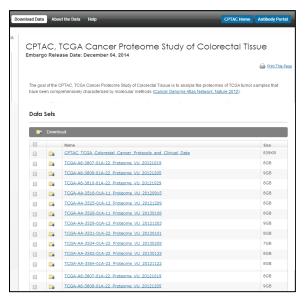
- Standardization of MS-based proteomic assays
  - Discovery (reference materials, MS QC software)
  - Verification: publicly available 510(k) mock documents using targeted immuno-MRM-MS assays
  - Experimental design considerations (power calculation, bias)
  - Standardization of monoclonal affinity reagents characterization generated for proteomics research
- Standardization of common data analysis pipeline (NIST): beneficial for reporting of multi-institutional TCGA proteomic results to the public (PSMs)

## **CPTAC Public Resources (Standardization)**





11,419 files (2.2 TB)

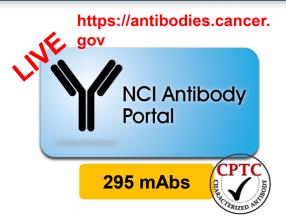


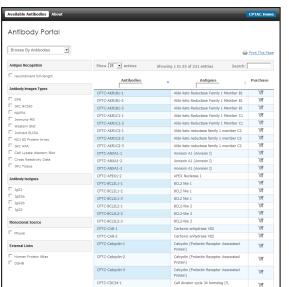


CrCa – completed

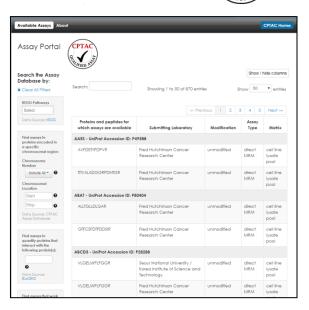
BrCa - completed

OvCa - 7/2014











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